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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/067,800

DATE: 02/26/2002

TIME: 13:20:13

Input Set : A:\seqlist 1488 115-I ascii

Output Set: N:\CRF3\02262002\J067800.raw

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5 <110> APPLICANT: Roschke, Viktor
6     Rosen, Craig A.
7     Ruben, Steven, M.
10 <120> TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
13 <130> FILE REFERENCE: 1488.115000I
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/067,800
C--> 15 <141> CURRENT FILING DATE: 2002-02-08
15 <150> PRIOR APPLICATION NUMBER: PCT/US01/04153
16 <151> PRIOR FILING DATE: 2001-02-09
18 <150> PRIOR APPLICATION NUMBER: 09/779,880
19 <151> PRIOR FILING DATE: 2001-02-09
21 <150> PRIOR APPLICATION NUMBER: 60/297,257
22 <151> PRIOR FILING DATE: 2001-06-12
24 <150> PRIOR APPLICATION NUMBER: 60/310,458
25 <151> PRIOR FILING DATE: 2001-08-08
27 <150> PRIOR APPLICATION NUMBER: 60/328,447
28 <151> PRIOR FILING DATE: 2001-10-12
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31 <151> PRIOR FILING DATE: 2001-12-21
33 <160> NUMBER OF SEQ ID NOS: 70
35 <170> SOFTWARE: PatentIn version 3.1
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40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
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44 <221> NAME/KEY: CDS
45 <222> LOCATION: (259)..(1314)
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52 ttaattcaat gtagacatct atgtaggcaa ttaaaaaacct attgatgtat aaaacagttt      180
54 gcattcatgg agggcaacta aatacattct aggactttat aaaagatcac tttttattta      240
56 tgcacagggt ggaacaag atg gat tat caa gtg tca agt cca atc tat gac      291
57                               Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp
58                               1             5             10
60 atc aat tat tat aca tcg gag ccc tgc cca aaa atc aat gtg aag caa      339
61 Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln
62             15             20             25
64 atc gca gcc cgc ctc ctg cct ccg ctc tac tca ctg gtg ttc atc ttt      387
65 Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe
66             30             35             40
68 ggt ttt gtg ggc aac atg ctg gtc atc ctc atc ctg ata aac tgc caa      435

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70      45                      50                      55
72 agg ctg gag agc atg act gac atc tac ctg ctc aac ctg gcc atc tct      483
73 Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser
74 60                      65                      70                      75
76 gac ctg ttt ttc ctt ctt act gtc ccc ttc tgg gct cac tat gct gcc      531
77 Asp Leu Phe Phe Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala
78      80                      85                      90
80 gcc cag tgg gac ttt gga aat aca atg tgt caa ctc ttg aca ggg ctc      579
81 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu
82      95                      100                      105
84 tat ttt ata ggc ttc ttc tct gga atc ttc ttc atc atc ctc ctg aca      627
85 Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr
86      110                      115                      120
88 atc gat agg tac ctg gct atc gtc cat gct gtg ttt gct tta aaa gcc      675
89 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala
90      125                      130                      135
92 agg acg gtc acc ttt ggg gtg gtg aca agt gtg atc act tgg gtg gtg      723
93 Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val
94 140                      145                      150                      155
96 gct gtg ttt gcg tct ctc cca gga atc atc ttt acc aga tct caa aaa      771
97 Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys
98      160                      165                      170
100 gaa ggt ctt cat tac acc tgc agc tct cat ttt cca tac agt cag tat      819
101 Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr
102      175                      180                      185
104 caa ttc tgg aag aat ttc cag aca tta aag ata gtc atc ttg ggg ctg      867
105 Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu
106      190                      195                      200
108 gtc ctg ccg ctg ctt gtc atg gtc atc tgc tac tcg gga atc cta aaa      915
109 Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys
110      205                      210                      215
112 act ctg ctt cgg tgt cga aat gag aag aag agg cac agg gct gtg agg      963
113 Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg
114 220                      225                      230                      235
116 ctt atc ttc acc atc atg att gtt tat ttt ctc ttc tgg gct ccc tac      1011
117 Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr
118      240                      245                      250
120 aac att gtc ctt ctc ctg aac acc ttc cag gaa ttc ttt ggc ctg aat      1059
121 Asn Ile Val Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn
122      255                      260                      265
124 aat tgc agt agc tct aac agg ttg gac caa gct atg cag gtg aca gag      1107
125 Asn Cys Ser Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu
126      270                      275                      280
128 act ctt ggg atg acg cac tgc tgc atc aac ccc atc atc tat gcc ttt      1155
129 Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe
130      285                      290                      295
132 gtc ggg gag aag ttc aga aac tac ctc tta gtc ttc ttc caa aag cac      1203
133 Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His

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136 att gcc aaa cgc ttc tgc aaa tgc tgt tct att ttc cag caa gag gct      1251
137 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala
138          320          325          330
140 ccc gag cga gca agc tca gtt tac acc cga tcc act ggg gag cag gaa      1299
141 Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu
142          335          340          345
144 ata tct gtg ggc ttg tgacacggac tcaagtgggc tgggtgacca gtcagagttg      1354
145 Ile Ser Val Gly Leu
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154 <212> TYPE: PRT
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159 1          5          10          15
161 Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
162          20          25          30
164 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
165          35          40          45
167 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln Arg Leu Glu Ser Met
168          50          55          60
170 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
171 65          70          75          80
173 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
174          85          90          95
176 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
177          100          105          110
179 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
180          115          120          125
182 Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
183          130          135          140
185 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
186 145          150          155          160
188 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
189          165          170          175
191 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
192          180          185          190
194 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195          195          200          205
197 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
198          210          215          220
200 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
201 225          230          235          240
203 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
204          245          250          255
206 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser

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209 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
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212 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
213          290          295          300
215 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
216 305          310          315          320
218 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
219          325          330          335
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253 <212> TYPE: DNA
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256 <220> FEATURE:
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264 <211> LENGTH: 61
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268 <220> FEATURE:
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274 c 61
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291 <212> TYPE: DNA
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294 <220> FEATURE:
295 <223> OTHER INFORMATION: 3' Oligonucleotide primer for HDGNR10
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302 <211> LENGTH: 344
303 <212> TYPE: PRT
304 <213> ORGANISM: Homo sapiens
306 <400> SEQUENCE: 9
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308 1 5 10 15
310 Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr
311 20 25 30
313 Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu
314 35 40 45
316 Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu
317 50 55 60
319 Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu
320 65 70 75 80
322 Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys
323 85 90 95
325 Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe
326 100 105 110
328 Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala
329 115 120 125
331 Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser
332 130 135 140
334 Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile
335 145 150 155 160
337 Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr
338 165 170 175
340 Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu
341 180 185 190
343 Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile
344 195 200 205
346 Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala
347 210 215 220
349 Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr
350 225 230 235 240
352 Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly
353 245 250 255
355 Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val

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PATENT APPLICATION: US/10/067,800

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